

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/663,618A

1814

#8

DATE: 06/16/97
TIME: 19:27:17

INPUT SET: S18386.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

- (i) APPLICANT: Gray, Patrick W.
- (ii) TITLE OF INVENTION: Chitinase Materials and Methods
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Rin-Laures, Li-Hsien
 - (B) REGISTRATION NUMBER: 33,547
 - (C) REFERENCE/DOCKET NUMBER: 27866/32960
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 312/474-6300
 - (B) TELEFAX: 312/474-0448
 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1636 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

RAW SEQUENCE LISTING

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47
48 (ii) MOLECULE TYPE: cDNA
49
50 (ix) FEATURE:
51 (A) NAME/KEY: CDS
52 (B) LOCATION: 2..1399
53
54 (ix) FEATURE:
55 (A) NAME/KEY: mat_peptide
56 (B) LOCATION: 65..1399
57
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60 C ATG GTG CGG TCT GTG GCC TGG GCA GGT TTC ATG GTC CTG CTG ATG 46
61 Met Val Arg Ser Val Ala Trp Ala Gly Phe Met Val Leu Leu Met
62 -21 -20 -15 -10
63
64 ATC CCA TGG GGC TCT GCT GCA AAA CTG GTC TGC TAC TTC ACC AAC TGG 94
65 Ile Pro Trp Gly Ser Ala Ala Lys Leu Val Cys Tyr Phe Thr Asn Trp
66 -5 1 5 10
67
68 GCC CAG TAC AGA CAG GGG GAG GCT CGC TTC CTG CCC AAG GAC TTG GAC 142
69 Ala Gln Tyr Arg Gln Gly Glu Ala Arg Phe Leu Pro Lys Asp Leu Asp
70 15 20 25
71
72 CCC AGC CTT TGC ACC CAC CTC ATC TAC GCC TTC GCT GGC ATG ACC AAC 190
73 Pro Ser Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn
74 30 35 40
75
76 CAC CAG CTG AGC ACC ACT GAG TGG AAT GAC GAG ACT CTC TAC CAG GAG 238
77 His Gln Leu Ser Thr Thr Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu
78 45 50 55
79
80 TTC AAT GGC CTG AAG AAG ATG AAT CCC AAG CTG AAG ACC CTG TTA GCC 286
81 Phe Asn Gly Leu Lys Lys Met Asn Pro Lys Leu Lys Thr Leu Leu Ala
82 60 65 70
83
84 ATC GGA GGC TGG AAT TTC GGC ACT CAG AAG TTC ACA GAT ATG GTA GCC 334
85 Ile Gly Gly Trp Asn Phe Gly Thr Gln Lys Phe Thr Asp Met Val Ala
86 75 80 85 90
87
88 ACG GCC AAC AAC CGT CAG ACC TTT GTC AAC TCG GCC ATC AGG TTT CTG 382
89 Thr Ala Asn Asn Arg Gln Thr Phe Val Asn Ser Ala Ile Arg Phe Leu
90 95 100 105
91
92 CGC AAA TAC AGC TTT GAC GGC CTT GAC CTT GAC TGG GAG TAC CCA GGA 430
93 Arg Lys Tyr Ser Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly
94 110 115 120
95
96 AGC CAG GGG AGC CCT GCC GTA GAC AAG GAG CGC TTC ACA ACC CTG GTA 478
97 Ser Gln Gly Ser Pro Ala Val Asp Lys Glu Arg Phe Thr Thr Leu Val
98 125 130 135
99

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100	CAG GAC TTG GCC AAT GCC TTC CAG CAG GAA GCC CAG ACC TCA GGG AAG	526
101	Gln Asp Leu Ala Asn Ala Phe Gln Gln Glu Ala Gln Thr Ser Gly Lys	
102	140 145 150	
103		
104	GAA CGC CTT CTT CTG AGT GCA GCG GTT CCA GCT GGG CAG ACC TAT GTG	574
105	Glu Arg Leu Leu Leu Ser Ala Ala Val Pro Ala Gly Gln Thr Tyr Val	
106	155 160 165 170	
107		
108	GAT GCT GGA TAC GAG GTG GAC AAA ATC GCC CAG AAC CTG GAT TTT GTC	622
109	Asp Ala Gly Tyr Glu Val Asp Lys Ile Ala Gln Asn Leu Asp Phe Val	
110	175 180 185	
111		
112	AAC CTT ATG GCC TAC GAC TTC CAT GGC TCT TGG GAG AAG GTC ACG GGA	670
113	Asn Leu Met Ala Tyr Asp Phe His Gly Ser Trp Glu Lys Val Thr Gly	
114	190 195 200	
115		
116	CAT AAC AGC CCC CTC TAC AAG AGG CAA GAA GAG AGT GGT GCA GCA GCC	718
117	His Asn Ser Pro Leu Tyr Lys Arg Gln Glu Glu Ser Gly Ala Ala Ala	
118	205 210 215	
119		
120	AGC CTC AAC GTG GAT GCT GCT GTG CAA CAG TGG CTG CAG AAG GGG ACC	766
121	Ser Leu Asn Val Asp Ala Ala Val Gln Gln Trp Leu Gln Lys Gly Thr	
122	220 225 230	
123		
124	CCT GCC AGC AAG CTG ATC CTT GGC ATG CCT ACC TAC GGA CGC TCC TTC	814
125	Pro Ala Ser Lys Leu Ile Leu Gly Met Pro Thr Tyr Gly Arg Ser Phe	
126	235 240 245 250	
127		
128	ACA CTG GCC TCC TCA TCA GAC ACC AGA GTG GGG GCC CCA GCC ACA GGG	862
129	Thr Leu Ala Ser Ser Ser Asp Thr Arg Val Gly Ala Pro Ala Thr Gly	
130	255 260 265	
131		
132	TCT GGC ACT CCA GGC CCC TTC ACC AAG GAA GGA GGG ATG CTG GCC TAC	910
133	Ser Gly Thr Pro Gly Pro Phe Thr Lys Glu Gly Gly Met Leu Ala Tyr	
134	270 275 280	
135		
136	TAT GAA GTC TGC TCC TGG AAG GGG GCC ACC AAA CAG AGA ATC CAG GAT	958
137	Tyr Glu Val Cys Ser Trp Lys Gly Ala Thr Lys Gln Arg Ile Gln Asp	
138	285 290 295	
139		
140	CAG AAG GTG CCC TAC ATC TTC CGG GAC AAC CAG TGG GTG GGC TTT GAT	1006
141	Gln Lys Val Pro Tyr Ile Phe Arg Asp Asn Gln Trp Val Gly Phe Asp	
142	300 305 310	
143		
144	GAT GTG GAG AGC TTC AAA ACC AAG GTC AGC TAT CTG AAG CAG AAG GGA	1054
145	Asp Val Glu Ser Phe Lys Thr Lys Val Ser Tyr Leu Lys Gln Lys Gly	
146	315 320 325 330	
147		
148	CTG GGC GGG GCC ATG GTC TGG GCA CTG GAC TTA GAT GAC TTT GAC GGC	1102
149	Leu Gly Gly Ala Met Val Trp Ala Leu Asp Leu Asp Asp Phe Ala Gly	
150	335 340 345	
151		
152	TTC TCC TGC AAC CAG GGC CGA TAC CCC CTC ATC CAG ACG CTA CGG CAG	1150

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153 Phe Ser Cys Asn Gln Gly Arg Tyr Pro Leu Ile Gln Thr Leu Arg Gln
154                               350                               355                               360
155
156 GAA CTG AGT CTT CCA TAC TTG CCT TCA GGC ACC CCA GAG CTT GAA GTT      1198
157 Glu Leu Ser Leu Pro Tyr Leu Pro Ser Gly Thr Pro Glu Leu Glu Val
158           365                               370                               375
159
160 CCA AAA CCA GGT CAG CCC TCT GAA CCT GAG CAT GGC CCC AGC CCT GGA      1246
161 Pro Lys Pro Gly Gln Pro Ser Glu Pro Glu His Gly Pro Ser Pro Gly
162           380                               385                               390
163
164 CAA GAC ACG TTC TGC CAG GGC AAA GCT GAT GGG CTC TAT CCC AAT CCT      1294
165 Gln Asp Thr Phe Cys Gln Gly Lys Ala Asp Gly Leu Tyr Pro Asn Pro
166 395                               400                               405                               410
167
168 CGG GAA CGG TCC AGC TTC TAC AGC TGT GCA GCG GGG CGG CTG TTC CAG      1342
169 Arg Glu Arg Ser Ser Phe Tyr Ser Cys Ala Ala Gly Arg Leu Phe Gln
170           415                               420                               425
171
172 CAA AGC TGC CCG ACA GGC CTG GTG TTC AGC AAC TCC TGC AAA TGC TGC      1390
173 Gln Ser Cys Pro Thr Gly Leu Val Phe Ser Asn Ser Cys Lys Cys Cys
174           430                               435                               440
175
176 ACC TGG AAT TGAGTCGCTA AAGCCCCCTCC AGTCCCAGCT TTGAGGCTGG      1439
177 Thr Trp Asn
178           445
179
180 GCCCAGGATC ACTCTACAGC CTGCCTCCTG GGTTTTCCCT GGGGGCCGCA ATCTGGCTCC      1499
181
182 TGCAGGCCTT TCTGTGGTCT TCCTTTATCC AGGCTTTCTG CTCTCAGCCT TGCCTTCCTT      1559
183
184 TTTTCTGGGT CTCCTGGGCT GCCCCTTTCA CTTGCAAAAT AAATCTTTGG TTTGTGCCCC      1619
185
186 TCTTCCCAAA AAAAAAA      1636
187
188 (2) INFORMATION FOR SEQ ID NO:2:
189
190 (i) SEQUENCE CHARACTERISTICS:
191 (A) LENGTH: 466 amino acids
192 (B) TYPE: amino acid
193 (D) TOPOLOGY: linear
194
195 (ii) MOLECULE TYPE: protein
196
197 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
198
199 Met Val Arg Ser Val Ala Trp Ala Gly Phe Met Val Leu Leu Met Ile
200 -21 -20                               -15                               -10
201
202 Pro Trp Gly Ser Ala Ala Lys Leu Val Cys Tyr Phe Thr Asn Trp Ala
203 -5                               1                               5                               10
204
205 Gln Tyr Arg Gln Gly Glu Ala Arg Phe Leu Pro Lys Asp Leu Asp Pro

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	15	20	25
206			
207			
208	Ser Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn His		
209	30	35	40
210			
211	Gln Leu Ser Thr Thr Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu Phe		
212	45	50	55
213			
214	Asn Gly Leu Lys Lys Met Asn Pro Lys Leu Lys Thr Leu Leu Ala Ile		
215	60	65	70
216			
217	Gly Gly Trp Asn Phe Gly Thr Gln Lys Phe Thr Asp Met Val Ala Thr		
218	80	85	90
219			
220	Ala Asn Asn Arg Gln Thr Phe Val Asn Ser Ala Ile Arg Phe Leu Arg		
221	95	100	105
222			
223	Lys Tyr Ser Phe Asp Gly Leu Asp Leu Asp Trp Glu Tyr Pro Gly Ser		
224	110	115	120
225			
226	Gln Gly Ser Pro Ala Val Asp Lys Glu Arg Phe Thr Thr Leu Val Gln		
227	125	130	135
228			
229	Asp Leu Ala Asn Ala Phe Gln Gln Glu Ala Gln Thr Ser Gly Lys Glu		
230	140	145	150
231			
232	Arg Leu Leu Leu Ser Ala Ala Val Pro Ala Gly Gln Thr Tyr Val Asp		
233	160	165	170
234			
235	Ala Gly Tyr Glu Val Asp Lys Ile Ala Gln Asn Leu Asp Phe Val Asn		
236	175	180	185
237			
238	Leu Met Ala Tyr Asp Phe His Gly Ser Trp Glu Lys Val Thr Gly His		
239	190	195	200
240			
241	Asn Ser Pro Leu Tyr Lys Arg Gln Glu Glu Ser Gly Ala Ala Ala Ser		
242	205	210	215
243			
244	Leu Asn Val Asp Ala Ala Val Gln Gln Trp Leu Gln Lys Gly Thr Pro		
245	220	225	230
246			
247	Ala Ser Lys Leu Ile Leu Gly Met Pro Thr Tyr Gly Arg Ser Phe Thr		
248	240	245	250
249			
250	Leu Ala Ser Ser Ser Asp Thr Arg Val Gly Ala Pro Ala Thr Gly Ser		
251	255	260	265
252			
253	Gly Thr Pro Gly Pro Phe Thr Lys Glu Gly Gly Met Leu Ala Tyr Tyr		
254	270	275	280
255			
256	Glu Val Cys Ser Trp Lys Gly Ala Thr Lys Gln Arg Ile Gln Asp Gln		
257	285	290	295
258			

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SEQUENCE VERIFICATION REPORT
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Original Text